

Seq ID 1101

Database : N\_Geneseq\_8:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*
- 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4635	100.0	4635	6	AAD39663	Aad39663 Human pho
2	4635	100.0	4635	13	ADQ89085	Adq89085 Human uro
3	3684.6	79.5	4237	6	ABA96005	Aba96005 Human lip
4	3345.2	72.2	4941	6	ABV72132	Abv72132 Nucleotid
5	2838.4	61.2	6551	6	ABK12390	Abk12390 cDNA enco
6	2838.4	61.2	6551	12	ADK70341	Adk70341 Respirato
7	2358	50.9	5365	13	ABD33214	Abd33214 Murine ca
8	2161.4	46.6	2243	6	ABA94696	Aba94696 Human lip
9	1540.4	33.2	6946	10	ADL15056	Adl15056 Human mal
10	1412.6	30.5	1833	13	ABD33216	Abd33216 Human c

Database : GenEmbl:\*  
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 7: gb\_sts:\*  
 8: gb\_sy:\*  
 9: gb\_un:\*  
 10: gb\_vi:\*  
 11: gb\_ov:\*  
 12: gb\_htg:\*  
 13: gb\_in:\*  
 14: gb\_om:\*  
 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4635	100.0	4635	2	AR658532	AR658532 Sequence
2	3922	84.6	6453	5	AK122589	AK122589 Homo sapi
3	3684.6	79.5	4237	2	AX304472	AX304472 Sequence
4	3624	78.2	3624	2	AR658533	AR658533 Sequence
5	3345.2	72.2	4941	2	AX512952	AX512952 Sequence
6	3339.2	72.0	5450	5	AB007919	AB007919 Homo sapi
7	2838.8	61.2	4837	5	DQ176850	DQ176850 Homo sapi
8	2838.4	61.2	6551	2	AX392826	AX392826 Sequence
9	2573.2	55.5	3497	6	AY966876	AY966876 Mus muscu
10	2527.4	54.5	4411	5	AK074149	AK074149 Homo sapi
11	2501.8	54.0	5333	6	AK129147	AK129147 Mus muscu
12	2297	49.6	4001	5	BC043358	BC043358 Homo sapi

Database : Issued\_Patents\_NA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	4635	100.0	4635	3	US-09-927-112-1	Sequence 1, Appli
2	3624	78.2	3624	3	US-09-927-112-3	Sequence 3, Appli
3	308.6	6.7	2289	3	US-10-258-860-1	Sequence 1, Appli
4	301.8	6.5	2211	3	US-09-800-971-3	Sequence 3, Appli
5	301.8	6.5	3425	3	US-09-800-971-1	Sequence 1, Appli
6	289.8	6.3	2627	4	US-09-880-107-3293	Sequence 3293, Ap
7	286.6	6.2	2752	3	US-10-104-047-135	Sequence 135, App
8	278.8	6.0	2627	3	US-09-949-016-5110	Sequence 5110, Ap
9	276.2	6.0	2462	3	US-10-258-860-5	Sequence 5, Appli
10	276.2	6.0	2540	3	US-10-258-860-3	Sequence 3, Appli
11	212.8	4.6	2958	3	US-09-688-078-5	Sequence

Database : Published\_Applications\_NA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4635	100.0	4635	3	US-09-927-112-1	Sequence 1, Appli
2	4635	100.0	4635	9	US-10-757-262-37	Sequence 37, Appl
3	4635	100.0	4635	9	US-10-784-089-1	Sequence 1, Appli
4	3684.6	79.5	4237	8	US-10-275-998-10	Sequence 10, Appl
5	3624	78.2	3624	3	US-09-927-112-3	Sequence 3, Appli
6	3624	78.2	3624	9	US-10-784-089-3	Sequence 3, Appli
7	3345.2	72.2	4941	8	US-10-467-248-15	Sequence 15, Appl
8	2838.4	61.2	6551	8	US-10-362-628-12	Sequence 12, Appl
9	2358	50.9	5365	8	US-10-322-281-224	Sequence 224, App
10	2161.4	46.6	2243	8	US-10-332-426-10	Sequence 10, Appl
11	1412.6	30.5	1833	8	US-10-322-281-227	Sequence 227, App
12	1127	24.3	3283	7	US-10-108-260A-1395	Sequence 1395, Ap
13	1111.2	24.0	3433	8	US-10-398-663-9	Sequence 9, Appli

Database : Published\_Applications\_NA\_New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq1:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq2:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2358	50.9	5365	6	US-10-539-228-224	Sequence 224, App
2	1412.6	30.5	1833	6	US-10-539-228-227	Sequence 227, App
3	1127	24.3	3283	8	US-11-293-697-1395	Sequence 1395, Ap
4	1103	23.8	3585	8	US-11-266-748A-32259	Sequence 32259, A
5	571.2	12.3	715	8	US-11-266-748A-366378	Sequence 366378,
c 6	571.2	12.3	715	8	US-11-266-748A-449757	Sequence 449757,
7	535.4	11.6	80105	6	US-10-539-228-223	Sequence 223, App
c 8	464.4	10.0	513	8	US-11-266-748A-104368	Sequence 104368,
9	464.4	10.0	513	8	US-11-266-748A-157179	Sequence 157179,
10	308.6	6.7	3107	8	US-11-266-748A-30946	Sequence 30946, A
11	308.6	6.7	3107	8	US-11-266-748A-56285	Sequence 56285, A
12	301.8	6.5	3445	8	US-11-266-748A-28175	Sequence 28175, A
13	301.8	6.5	5926	8	US-11-266-748A-22592	Sequence 22592, A
14	300.2	6.5	2773	8	US-11-266-748A-57630	Sequence 57630

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est3:\*
- 3: gb\_est4:\*
- 4: gb\_est5:\*
- 5: gb\_est6:\*
- 6: gb\_htc:\*
- 7: gb\_est2:\*
- 8: gb\_est7:\*
- 9: gb\_est8:\*
- 10: gb\_est9:\*
- 11: gb\_gss1:\*
- 12: gb\_gss2:\*
- 13: gb\_gss3:\*
- 14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	%		Query		DB	ID	Description
	Score	Match	Length				
1	2548	55.0	5324	6	AK044619	AK044619 Mus muscu	
2	1307.6	28.2	1836	6	AK049970	AK049970 Mus muscu	
3	1170.6	25.3	1817	6	AK078731	AK078731 Mus muscu	
4	920.2	19.9	947	14	DQ035829	DQ035829 Homo sapi	
5	808	17.4	1278	14	DQ035827	DQ035827 Homo sapi	
6	717.4	15.5	857	14	DQ035830	DQ035830 Pan trogl	
7	693.8	15.0	886	10	DV878798	DV878798 LB0263.CR	
8	669.2	14.4	692	8	CR998048	CR998048 CR998048	
9	647	14.0	889	3	BQ946757	BQ946757 AGENCOURT	
10	644.6	13.9	958	3	BU159213	BU159213 AGENCOURT	
11	627	13.5	759	5	CF531476	CF531476 UI-M-FY0-	
12	626.6	13.5	763	5	CF531795	CF531795 UI-M-FY0-	
13	620	13.4	1092	3	BU502871	BU502871 AGENCOURT	

Seq ID 10: 3

Database : GenEmbl:\*

- 1: gb\_env:\*
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- 3: gb\_ph:\*
- 4: gb\_pl:\*
- 5: gb\_pr:\*
- 6: gb\_ro:\*
- 7: gb\_sts:\*
- 8: gb\_sy:\*
- 9: gb\_un:\*
- 10: gb\_vi:\*
- 11: gb\_ov:\*
- 12: gb\_htg:\*
- 13: gb\_in:\*
- 14: gb\_om:\*
- 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3624	100.0	3624	2	AR658533	AR658533 Sequence
2	3624	100.0	4635	2	AR658532	AR658532 Sequence
3	3360.2	92.7	6453	5	AK122589	AK122589 Homo sapi
4	3345.2	92.3	4941	2	AX512952	AX512952 Sequence
5	3339.2	92.1	5450	5	AB007919	AB007919 Homo sapi
6	3269.2	90.2	4237	2	AX304472	AX304472 Sequence
7	2838.8	78.3	4837	5	DQ176850	DQ176850 Homo sapi
8	2838.4	78.3	6551	2	AX392826	AX392826 Sequence
9	2573.2	71.0	3497	6	AY966876	AY966876 Mus muscu
10	2501.8	69.0	5333	6	AK129147	AK129147 Mus muscu
11	2297	63.4	4001	5	BC043358	BC043358 Homo sapi
12	2265.4	62.5	4791	6	DQ176851	DQ176851 Mus muscu
13	1965.6	54.2	4411	5	AK074149	AK074149 Homo sapi
14	1914.4	52.8	2697	2	CQ721801	CQ721801 Sequence
15	1840	50.8	2243	2	AX402958	AX402958

RESULT 7  
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VERSION DQ176850.1 GI:74486662  
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ORGANISM Homo sapiens  
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Hominidae; Homo.  
REFERENCE 1 (bases 1 to 4837)  
AUTHORS Zhou,Y., Wing,M.R., Sondek,J. and Harden,T.K.  
TITLE Molecular cloning and characterization of phospholipase C-eta2  
JOURNAL (er) Biochem. J. (2005) In press  
REFERENCE 2 (bases 1 to 4837)  
AUTHORS Zhou,Y., Wing,M.R., Sondek,J. and Harden,T.K.  
TITLE Direct Submission  
JOURNAL Submitted (23-AUG-2005) Pharmacology, UNC Chapel Hill, 1106 ME  
Jones Building (CB#7365), Chapel Hill, NC 27599, USA  
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3' UTR

Query Match 78.3%; Score 2838.8; DB 5; Length 4837;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2840; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

http://es/ScoreAccessWeb/GetItem.action?ApplId=10784089&seqId=608582&ItemName=us... 9/19/06

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Db	1112	AGCTGCCAGGACATCATCGAGCAGTTTGAGCCATGCCAGAAAACAAGAGTAAGGGGCTG	1171
Qy	886	CTGGGCATTGATGGCTTCAACCACTACACCAGGAGCCCTGCTGGTGACATCTTCAACCCT	945
Db	1172	CTGGGCATTGATGGCTTCAACCACTACACCAGGAGCCCTGCTGGTGACATCTTCAACCCT	1231
Qy	946	GAGCACCACCATGTGCAACCAGGACATGACGCAGCCGCTGAGCCACTACTTCATCACCTCG	1005
Db	1232	GAGCACCACCATGTGCAACCAGGACATGACGCAGCCGCTGAGCCACTACTTCATCACCTCG	1291
Qy	1006	TCCCACAACACCTACCTCGTGGGTGACCAGCTCATGTCCCAGTCACGGGTGGACATGTAT	1065
Db	1292	TCCCACAACACCTACCTCGTGGGTGACCAGCTCATGTCCCAGTCACGGGTGGACATGTAT	1351
Qy	1066	GCTTGGGTCCTGCAGGCTGGCTGCCGCTGCGTGGAGGTGGACTGCTGGGATGGGCCCGAC	1125
Db	1352	GCTTGGGTCCTGCAGGCTGGCTGCCGCTGCGTGGAGGTGGACTGCTGGGATGGGCCCGAC	1411
Qy	1126	GGGGAGCCCATTTGTGCACCATGGCTA CACTCTGACTTCCAAGATCCTCTTCAAAGACGTC	1185
Db	1412	GGGGAGCCCATTTGTGCACCATGGCTA CACTCTGACTTCCAAGATCCTCTTCAAAGACGTC	1471
Qy	1186	ATTGAAACCATCAACAAATATGCCTTCATCAAGAATGAGTACCCAGTGATCCTGTCCATC	1245
Db	1472	ATTGAAACCATCAACAAATATGCCTTCATCAAGAATGAGTACCCAGTGATCCTGTCCATC	1531
Qy	1246	GAAAACCACTGCAGTGT CATCCAGCAGAAGAAAATGGCCCAGTATCTGACTGACATCCTT	1305
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Qy	1306	GGGGACAAGCTGGACCTGT CATCAGTGAGCAGTGAAGATGCCACCACACTCCCCTCTCCA	1365
Db	1592	GGGGACAAGCTGGACCTGT CATCAGTGAGCAGTGAAGATGCCACCACACTCCCCTCTCCA	1651
Qy	1366	CAGATGCTCAAGGGCAAGATCCTCGTGAAGGGGAAGAAGCTCCCAGCCAACATCAGCGAG	1425
Db	1652	CAGATGCTCAAGGGCAAGATCCTCGTGAAGGGGAAGAAGCTCCCAGCCAACATCAGCGAG	1711
Qy	1426	GATGCGGAGGAAGGCGAGGTGTCTGATGAGGACAGTGCTGATGAGATTGACGATGACTGC	1485
Db	1712	GATGCGGAGGAAGGCGAGGTGTCTGATGAGGACAGTGCTGATGAGATTGACGATGACTGC	1771
Qy	1486	AAGCTCCTCAATGGGGATGCATCCACCAATCGAAAGCGTGTAGAAAACACTGCTAAGAGG	1545
Db	1772	AAGCTCCTCAATGGGGATGCATCCACCAATCGAAAGCGTGTAGAAAACACTGCTAAGAGG	1831
Qy	1546	AAACTGGATTCCCTCATCAAAGAGTCGAAGATTCTGGGACTGTGAGGACCCCAACAACCTC	1605
Db	1832	AAACTGGATTCCCTCATCAAAGAGTCGAAGATTCTGGGACTGTGAGGACCCCAACAACCTC	1891
Qy	1606	TCCGTCTCCACACTGTCCCATCTGGAAAGCTCGGACGCAAGAGCAAGGCTGAAGAGGAC	1665
Db	1892	TCCGTCTCCACACTGTCCCATCTGGAAAGCTCGGACGCAAGAGCAAGGCTGAAGAGGAC	1951
Qy	1666	GTGGAGTCTGGGGAGGATGCCGGGGCCAGCAGACGCAATGGCCGCTCGTCTGGGAAGC	1725
Db	1952	GTGGAGTCTGGGGAGGATGCCGGGGCCAGCAGACGCAATGGCCGCTCGTCTGGGAAGC	2011
Qy	1726	TTCTCCAGGCGCAAGAAGAAGGGCAGCAAGCTGAAGAAGGCGCCAGCGTGGAGGAGGGA	1785

Db	2012	 TTCTCCAGGCGCAAGAAGAAGGGCAGCAAGCTGAAGAAGGCGCCAGCGTGGAGGAGGGA	2071
Qy	1786	GATGAGGGTCAGGACTCCCCGGGAGGCCAGAGCCGAGGGGCGACCCGGCAGAAGAAGACC	1845
Db	2072	 GATGAGGGTCAGGACTCCCCGGGAGGCCAGAGCCGAGGGGCGACCCGGCAGAAGAAGACC	2131
Qy	1846	ATGAAGCTGTCCCGGGCCCTCTCTGACCTGGTGAAGTACACCAAGTCCGTGGCCACCCAC	1905
Db	2132	 ATGAAGCTGTCCCGGGCCCTCTCTGACCTGGTGAAGTACACCAAGTCCGTGGCCACCCAC	2191
Qy	1906	GACATAGAGATGGAGGCGGCGTCCAGCTGGCAGGTGTCGTCCTTCAGCGAGACCAAGGCC	1965
Db	2192	 GACATAGAGATGGAGGCGGCGTCCAGCTGGCAGGTGTCGTCCTTCAGCGAGACCAAGGCC	2251
Qy	1966	CACCAGATTCTGCAGCAGAAGCCGGCGCAGTACCTACGCTTCAACCAGCAGCAGCTCTCC	2025
Db	2252	 CACCAGATTCTGCAGCAGAAGCCGGCGCAGTACCTACGCTTCAACCAGCAGCAGCTCTCC	2311
Qy	2026	CGCATCTACCCCTCCTCCTACCGTGTGGACTCCAGCAACTACAACCCGAGCCCTTCTGG	2085
Db	2312	 CGCATCTACCCCTCCTCCTACCGTGTGGACTCCAGCAACTACAACCCGAGCCCTTCTGG	2371
Qy	2086	AACGCCGGCTGCCAAATGGTTGCCCTGAACTACCAGTCAGAGGGGCGGATGCTGCAGCTG	2145
Db	2372	 AACGCCGGCTGCCAAATGGTTGCCCTGAACTACCAGTCAGAGGGGCGGATGCTGCAGCTG	2431
Qy	2146	AACCGAGCCAAGTTCAGCGCCAACGGTGGCTGCGGCTACGTACTCAAGCCTGGGTGCATG	2205
Db	2432	 AACCGAGCCAAGTTCAGCGCCAACGGTGGCTGCGGCTACGTACTCAAGCCTGGGTGCATG	2491
Qy	2206	TGCCAGGGCGTGTTCACCCCAACTCGGAGGACCCCTGCCCGGGCAGCTCAAGAAGCAG	2265
Db	2492	 TGCCAGGGCGTGTTCACCCCAACTCGGAGGACCCCTGCCCGGGCAGCTCAAGAAGCAG	2551
Qy	2266	CTGGTGCTCCGGATCATCAGTGGCCAGCAGCTTCCCAAGCCGCGCGACTCCATGCTGGGG	2325
Db	2552	 CTGGTGCTCCGGATCATCAGTGGCCAGCAGCTTCCCAAGCCGCGCGACTCCATGCTGGGG	2611
Qy	2326	GACCGTGGGGAGATCATCGACCCCTTTGTGGAGGTGGAGATCATTTGGGCTCCCTGTGGAC	2385
Db	2612	 GACCGTGGGGAGATCATCGACCCCTTTGTGGAGGTGGAGATCATTTGGGCTCCCTGTGGAC	2671
Qy	2386	TGCAGCAGGGAGCAGACCCGCGTGGTGGACGACAACGGTTCAACCCACCTGGGAGGAG	2445
Db	2672	 TGCAGCAGGGAGCAGACCCGCGTGGTGGACGACAACGGTTCAACCCACCTGGGAGGAG	2731
Qy	2446	ACCCTGGTTTTTCATGGTGCACATGCCGAGATCGCGTGGTCCGCTTCCTCGTCTGGGAC	2505
Db	2732	 ACCCTGGTTTTTCATGGTGCACATGCCGAGATCGCGTGGTCCGCTTCCTCGTCTGGGAC	2791
Qy	2506	CACGATCCCATCGGGCGTGACTTCATTGGCCAGAGGACGCTGGCCTTCAGCAGCATGATG	2565
Db	2792	 CACGATCCCATCGGGCGTGACTTCATTGGCCAGAGGACGCTGGCCTTCAGCAGCATGATG	2851
Qy	2566	CCAGGCTACAGACACGTGTACCTAGAAGGGATGGAAGAGGCTCCATCTTCGTGCATGTG	2625
Db	2852	 CCAGGCTACAGACACGTGTACCTAGAAGGGATGGAAGAGGCTCCATCTTCGTGCATGTG	2911
Qy	2626	GCTGTCAGTGACATCAGCGGTAAGGTCAAGCAGGCTCTGGGCCTAAAAGGCCTCTTCCTC	2685

Db	2912	GCTGTCAGTGACATCAGCGGTAAGGTCAAGCAGGCTCTGGGCCTAAAAGGCCTCTTCCTC	2971
Qy	2686	CGAGGCCCAAAGCCCGGCTCGCTGGACAGTCATGCTGCTGGGCGGCCCCCGGCCCGGCC	2745
Db	2972	CGAGGCCCAAAGCCCGGCTCGCTGGACAGTCATGCTGCTGGGCGGCCCCCGGCCCGGCC	3031
Qy	2746	TCCGTTAGCCAGCGGATCCTGCGGCGCACGGCCAGCGCCCGACCAAGAGCCAGAAGCCG	2805
Db	3032	TCCGTTAGCCAGCGGATCCTGCGGCGCACGGCCAGCGCCCGACCAAGAGCCAGAAGCCG	3091
Qy	2806	GGCCGCAGGGGCTTCCCGGAGCTGGTCTGGGTACACGGGACACAGGCTCCAAGGGGGTG	2865
Db	3092	GGCCGCAGGGGCTTCCCGGAGCTGGTCTGGGTACACGGGACACAGGCTCCAAGGGGGTG	3151
Qy	2866	GCAGACGATGTGGTGCCCCCGGGCCCGGACCTGCTCCGGAAGCCCCAGCCCAGGAGGGG	2925
Db	3152	GCAGACGATGTGGTGCCCCCGGGCCCGGACCTGCTCCGGAAGCCCCAGCCCAGGAGGGG	3211
Qy	2926	CCCGGCAGCGGCAGCCCCCGAG	2947
Db	3212	CCCGGCAGCGGCAGCCCCCGAG	3233

Database : Issued Patents\_NA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	3624	100.0	3624	3	US-09-927-112-3	Sequence 3, Appli
2	3624	100.0	4635	3	US-09-927-112-1	Sequence 1, Appli
3	308.6	8.5	2289	3	US-10-258-860-1	Sequence 1, Appli
4	301.8	8.3	2211	3	US-09-800-971-3	Sequence 3, Appli
5	301.8	8.3	3425	3	US-09-800-971-1	Sequence 1, Appli
6	289.8	8.0	2627	4	US-09-880-107-3293	Sequence 3293, Ap
7	286.6	7.9	2752	3	US-10-104-047-135	Sequence 135, App
8	278.8	7.7	2627	3	US-09-949-016-5110	Sequence 5110, Ap
9	276.2	7.6	2462	3	US-10-258-860-5	Sequence 5, Appli
10	276.2	7.6	2540	3	US-10-258-860-3	Sequence 3, Appli
11	212.8	5.9	2958	3	US-09-688-078-5	Sequence 5, Appli
12	201.2	5.6	4147	3	US-09-688-078-6	Sequence 6, Appli
13	200.8	5.5	3006	3	US-09-688-078-1	Sequence 1, Appli
14	200.8	5.5	3238	3	US-09-688-078-8	Sequence 8, Appli
15	194.4	5.4	4543	3	US-09-949-002-135	Sequence 135, App
16	194.4	5.4	185765	3	US-09-949-002-674	Sequence 674, App

Database : Published\_Applications\_NA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3624	100.0	3624	3	US-09-927-112-3	Sequence 3, Appli
2	3624	100.0	3624	9	US-10-784-089-3	Sequence 3, Appli
3	3624	100.0	4635	3	US-09-927-112-1	Sequence 1, Appli
4	3624	100.0	4635	9	US-10-757-262-37	Sequence 37, Appl
5	3624	100.0	4635	9	US-10-784-089-1	Sequence 1, Appli
6	3345.2	92.3	4941	8	US-10-467-248-15	Sequence 15, Appl
7	3269.2	90.2	4237	8	US-10-275-998-10	Sequence 10, Appl
8	2838.4	78.3	6551	8	US-10-362-628-12	Sequence 12, Appl
9	2358	65.1	5365	8	US-10-322-281-224	Sequence 224, App
10	1840	50.8	2243	8	US-10-332-426-10	Sequence 10, Appl
11	1412.6	39.0	1833	8	US-10-322-281-227	Sequence 227, App
12	1127	31.1	3283	7	US-10-108-260A-1395	Sequence 1395, Ap
13	1111.2	30.7	3433	8	US-10-398-663-9	Sequence

Database : Published\_Applications\_NA\_New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq1:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq2:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	2358	65.1	5365	6	US-10-539-228-224	Sequence 224, App
2	1412.6	39.0	1833	6	US-10-539-228-227	Sequence 227, App
3	1127	31.1	3283	8	US-11-293-697-1395	Sequence 1395, Ap
4	1103	30.4	3585	8	US-11-266-748A-32259	Sequence 32259, A
5	571.2	15.8	715	8	US-11-266-748A-366378	Sequence 366378,
c 6	571.2	15.8	715	8	US-11-266-748A-449757	Sequence 449757,
7	535.4	14.8	80105	6	US-10-539-228-223	Sequence 223, App
c 8	464.4	12.8	513	8	US-11-266-748A-104368	Sequence 104368,
9	464.4	12.8	513	8	US-11-266-748A-157179	Sequence 157179,
10	308.6	8.5	3107	8	US-11-266-748A-30946	Sequence 30946, A
11	308.6	8.5	3107	8	US-11-266-748A-56285	Sequence 56285, A
12	301.8	8.3	3445	8	US-11-266-748A-28175	Sequence 28175, A
13	301.8	8.3	5926	8	US-11-266-748A-22592	Sequence 22592, A
14	300.2	8.3	2773	8	US-11-266-748A-57630	Sequence 57630, A
15	244.4	6.7	43865	6	US-10-539-228-226	Sequence

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est3:\*
- 3: gb\_est4:\*
- 4: gb\_est5:\*
- 5: gb\_est6:\*
- 6: gb\_htc:\*
- 7: gb\_est2:\*
- 8: gb\_est7:\*
- 9: gb\_est8:\*
- 10: gb\_est9:\*
- 11: gb\_gss1:\*
- 12: gb\_gss2:\*
- 13: gb\_gss3:\*
- 14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2548	70.3	5324	6	AK044619	AK044619 Mus muscu
2	1307.6	36.1	1836	6	AK049970	AK049970 Mus muscu
3	1170.6	32.3	1817	6	AK078731	AK078731 Mus muscu
4	920.2	25.4	947	14	DQ035829	DQ035829 Homo sapi
5	808	22.3	1278	14	DQ035827	DQ035827 Homo sapi
6	717.4	19.8	857	14	DQ035830	DQ035830 Pan trogl
7	693.8	19.1	886	10	DV878798	DV878798 LB0263.CR
8	669.2	18.5	692	8	CR998048	CR998048 CR998048
9	647	17.9	889	3	BQ946757	BQ946757 AGENCOURT
10	644.6	17.8	958	3	BU159213	BU159213 AGENCOURT
11	627	17.3	759	5	CF531476	CF531476 UI-M-FY0-
12	626.6	17.3	763	5	CF531795	CF531795 UI-M-FY0-
13	620	17.1	1092	3	BU502871	BU502871 AGENCOURT
14	610.4	16.8	930	3	BQ960462	BQ960462 AGENCOURT



Database : N\_Geneseq\_8:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*
- 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3624	100.0	4635	6	AAD39663	Aad39663 Human pho
2	3624	100.0	4635	13	ADQ89085	Adq89085 Human uro
3	3345.2	92.3	4941	6	ABV72132	Abv72132 Nucleotid
4	3269.2	90.2	4237	6	ABA96005	Aba96005 Human lip
5	2838.4	78.3	6551	6	ABK12390	Abk12390 cDNA enco
6	2838.4	78.3	6551	12	ADK70341	Adk70341 Respirato
7	2358	65.1	5365	13	ABD33214	Abd33214 Murine ca
8	1840	50.8	2243	6	ABA94696	Aba94696 Human lip
9	1412.6	39.0	1833	13	ABD33216	Abd33216 Human can
10	1127	31.1	3283	11	ADM02710	Adm02710 Human cDN
11	1127	31.1	3283	14	AEC85640	Aec85640 Human cDN
12	1111.2	30.7	3433	6	ABL60537	Abl60537 Human

SEQ ID 10: 2

Database : A\_Geneseq\_8:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*
- 10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	6379	100.0	1207	5	AAE24599	Aae24599 Human pho
2	6379	100.0	1207	8	ADQ89086	Adq89086 Human uro
3	6092.5	95.5	1239	5	ABB08205	Abb08205 Human lip
4	5847.5	91.7	1152	5	ABB78295	Abb78295 Amino aci
5	5000	78.4	1605	8	ABO84827	Abo84827 Murine ca
6	4941	77.5	1619	5	AAU77498	Aau77498 Human lip
7	4941	77.5	1619	8	ADK70467	Adk70467 Respirato
8	3225	50.6	621	5	ABB07493	Abb07493 Human lip
9	3163	49.6	1014	5	ABB08001	Abb08001 Human lip
10	3161.5	49.6	968	7	ADM05153	Adm05153 Human pro
11	3161.5	49.6	968	9	AEC88083	Aec88083 Human cDN
12	2640	41.4	916	7	ADE47776	Ade47776 Human NOV
13	2640	41.4	916	8	ADJ79046	Adj79046 Human NOV
14	2343	36.7	787	4	ABG13669	Abg13669 Novel hum
15	2343	36.7	787	5	AAE14673	Aae14673 Human pho
16	2343	36.7	787	8	ADL61315	Adl61315 Human pro
17	2343	36.7	787	8	ADQ19653	Adq19653 Human sof

Database : Issued\_Patents\_AA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	6379	100.0	1207	2	US-09-927-112-2	Sequence 2, Appli
2	1738	27.2	325	2	US-09-927-112-10	Sequence 10, Appl
3	1578	24.7	1154	2	US-09-688-078-7	Sequence 7, Appli
4	1563.5	24.5	1001	2	US-09-688-078-2	Sequence 2, Appli
5	1526.5	23.9	1017	2	US-09-949-002-421	Sequence 421, App
6	1524.5	23.9	997	2	US-09-961-403-15	Sequence 15, Appl
7	1524.5	23.9	997	2	US-09-949-002-388	Sequence 388, App
8	1517.5	23.8	916	2	US-09-688-078-9	Sequence 9, Appli
9	1441	22.6	762	2	US-10-258-860-2	Sequence 2, Appli
10	1385.5	21.7	759	2	US-10-258-860-6	Sequence 6, Appli
11	1372.5	21.5	785	2	US-10-258-860-4	Sequence 4, Appli
12	1290.5	20.2	777	2	US-10-104-047-2105	Sequence 2105, Ap
13	1281	20.1	744	2	US-09-738-884-4	Sequence

Database : Published\_Applications\_AA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	6379	100.0	1207	3	US-09-927-112-2	Sequence 2, Appli
2	6379	100.0	1207	4	US-10-757-262-38	Sequence 38, Appl
3	6379	100.0	1207	5	US-10-784-089-2	Sequence 2, Appli
4	6092.5	95.5	1239	4	US-10-275-998-5	Sequence 5, Appli
5	5847.5	91.7	1152	4	US-10-467-248-6	Sequence 6, Appli
6	4981	78.1	1601	4	US-10-322-281-225	Sequence 225, App
7	4941	77.5	1619	4	US-10-362-628-6	Sequence 6, Appli
8	3225	50.6	621	4	US-10-332-426-2	Sequence 2, Appli
9	3163	49.6	1014	4	US-10-398-663-1	Sequence 1, Appli
10	3161.5	49.6	968	4	US-10-108-260A-3838	Sequence 3838, Ap
11	2640	41.4	916	4	US-10-210-130-138	Sequence 138, App
12	2343	36.7	787	4	US-10-648-593-239	Sequence 239, App
13	2343	36.7	787	5	US-10-723-860-2472	Sequence 2472, Ap
14	2343	36.7	787	5	US-10-756-149-5375	Sequence 5375, Ap
15	2343	36.7	787	5	US-10-450-763-44028	Sequence 44028, A
16	2343	36.7	787	6	US-11-072-175-239	Sequence 239, App

Database : Published\_Applications\_AA\_New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4981	78.1	1601	6	US-10-539-228-225	Sequence 225, App
2	3161.5	49.6	968	7	US-11-293-697-3838	Sequence 3838, Ap
3	1626.5	25.5	316	6	US-10-539-228-228	Sequence 228, App
4	997	15.6	1291	7	US-11-346-759-78	Sequence 78, Appl
5	955.5	15.0	1163	6	US-10-539-228-802	Sequence 802, App
6	927	14.5	1010	6	US-10-539-228-804	Sequence 804, App
7	900	14.1	1234	6	US-10-505-928-654	Sequence 654, App
8	840.5	13.2	1809	6	US-10-370-959-67	Sequence 67, Appl
9	773	12.1	403	7	US-11-293-697-4438	Sequence 4438, Ap
10	740	11.6	1057	6	US-10-539-228-799	Sequence 799, App
11	734.5	11.5	648	7	US-11-277-204-24	Sequence 24, Appl
12	604.5	9.5	553	6	US-10-953-349-15163	Sequence 15163, A
13	604.5	9.5	578	6	US-10-953-349-15162	Sequence 15162, A
14	593.5	9.3	598	6	US-10-449-902-48510	Sequence 48510, A
15	580.5	9.1	598	6	US-10-449-902-42757	Sequence 42757, A
16	580	9.1	617	6	US-10-449-902-50297	Sequence

Database : PIR\_80:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1524.5	23.9	997	1	I54390	phosphoinositide-s
2	1517	23.8	1096	1	S62358	inositol 1,4,5-tri
3	1459	22.9	764	1	S14113	1-phosphatidylinos
4	1358.5	21.3	753	2	JC8057	phospholipase C (E
5	1297	20.3	895	2	T32374	hypothetical prote
6	1287	20.2	745	1	PC4183	1-phosphatidylinos
7	1285	20.1	756	1	A55943	1-phosphatidylinos
8	1258	19.7	756	1	B28821	1-phosphatidylinos
9	1244	19.5	709	2	C28821	1-phosphatidylinos
10	1009	15.8	1291	2	S00666	1-phosphatidylinos
11	997.5	15.6	1290	2	A36466	1-phosphatidylinos
12	997	15.6	1176	1	A48047	phospholipase C (E
13	986	15.5	1236	1	A53970	1-phosphatidylinos
14	985	15.4	1290	2	A31317	1-phosphatidylinos
15	968.5	15.2	1265	2	A34163	1-phosphatidylinos
16	950.5	14.9	1252	2	S02004	phospholipase C (E
17	947.5	14.9	1312	1	B40879	phospholipase C (E
18	945	14.8	1216	2	A28821	1-phosphatidylinos
19	943	14.8	1305	2	A40879	phospholipase

Database : UniProt\_7.2:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	5893	92.4	1129	2	Q86YU9_HUMAN	Q86yu9 homo sapien
2	5852	91.7	1182	1	PLCL4_HUMAN	O75038 homo sapien
3	5576	87.4	1058	2	Q5TA87_HUMAN	Q5ta87 homo sapien
4	5149.5	80.7	1164	2	Q4QSC7_MOUSE	Q4qsc7 mus musculu
5	5047	79.1	1416	2	Q3LUA8_HUMAN	Q3lua8 homo sapien
6	4647.5	72.9	1501	2	Q3LUA7_MOUSE	Q3lua7 mus musculu
7	4113.5	64.5	1238	2	Q86XJ2_HUMAN	Q86xj2 homo sapien
8	3905.5	61.2	1168	2	Q5TA86_HUMAN	Q5ta86 homo sapien
9	3450	54.1	656	2	Q8TEH5_HUMAN	Q8teh5 homo sapien
10	3166.5	49.6	1682	2	Q4KWH5_MOUSE	Q4kwh5 mus musculu
11	3159.5	49.5	1002	2	Q4KWH9_HUMAN	Q4kwh9 homo sapien
12	3159.5	49.5	1693	2	Q4KWH8_HUMAN	Q4kwh8 homo sapien
13	3157	49.5	1003	2	Q4KWH7_MOUSE	Q4kwh7 mus musculu
14	3157	49.5	1073	2	Q4KWH6_MOUSE	Q4kwh6 mus

## RESULT 1

## Q86YU9\_HUMAN

ID Q86YU9\_HUMAN PRELIMINARY; PRT; 1129 AA.  
AC Q86YU9;  
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-2003, sequence version 1.  
DT 07-FEB-2006, entry version 17.  
DE FLJ00414 protein (Fragment).  
GN Name=FLJ00414;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;  
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.  
CC -!- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-  
CC bisphosphate + H(2)O = 1D-myo-inositol 1,4,5-trisphosphate +  
CC diacylglycerol.  
CC -!- SIMILARITY: Contains 1 C2 domain.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AK122589; BAC56930.1; -; mRNA.  
DR HSSP; P10688; 1DJX.  
DR Ensembl; ENSG00000149527; Homo sapiens.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004435; F:phosphoinositide phospholipase C activity; IEA.  
DR GO; GO:0004871; F:signal transducer activity; IEA.  
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
DR GO; GO:0016042; P:lipid catabolism; IEA.  
DR InterPro; IPR000008; C2.  
DR InterPro; IPR011992; EF-Hand\_type.  
DR InterPro; IPR002048; EF\_hand\_Ca\_bd.  
DR InterPro; IPR001849; PH.  
DR InterPro; IPR011993; PH\_type.  
DR InterPro; IPR001192; PI\_PLC.  
DR InterPro; IPR000909; PI\_PLC\_X.  
DR InterPro; IPR001711; PI\_PLC\_Y.  
DR Pfam; PF00168; C2; 1.  
DR Pfam; PF00036; efhand; 3.  
DR Pfam; PF00388; PI-PLC-X; 1.  
DR Pfam; PF00387; PI-PLC-Y; 1.  
DR PRINTS; PR00360; C2DOMAIN.  
DR PRINTS; PR00390; PHPLIPASEC.  
DR ProDom; PD000012; EF-hand; 1.  
DR ProDom; PD001202; PI\_PLC\_Y; 2.  
DR SMART; SM00239; C2; 1.  
DR SMART; SM00054; EFh; 2.  
DR SMART; SM00148; PLCXc; 1.  
DR SMART; SM00149; PLCYc; 1.  
DR PROSITE; PS50004; C2\_DOMAIN; 1.  
DR PROSITE; PS00018; EF\_HAND\_1; UNKNOWN\_1.  
DR PROSITE; PS50222; EF\_HAND\_2; 2.  
DR PROSITE; PS50003; PH\_DOMAIN; 1.  
DR PROSITE; PS50007; PIPLC\_X\_DOMAIN; 1.



DR PROSITE; PS50008; PIPLC\_Y\_DOMAIN; 1.  
 KW Calcium; Hydrolase; Lipid degradation; Transducer.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 1129 AA; 123498 MW; CBC23844616C5402 CRC64;

Query Match 92.4%; Score 5893; DB 2; Length 1129;  
 Best Local Similarity 99.7%; Pred. No. 6.6e-276;  
 Matches 1118; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	87	ISIDSIQEVSEGRQSEVFQRYPDGSFDPNCCFSIYHGSHRESLDLVSTSSSEVARTWVTGL	146
		:	
Db	9	VSIDSIQEVSEGRQSEVFQRYPDGSFDPNCCFSIYHGSHRESLDLVSTSSSEVARTWVTGL	68
Qy	147	RYLMAGISDEDSLARRQRTRDQWLKQTFDEADKNGDGSLSIGEVQLLHKLNVNLPQRV	206
Db	69	RYLMAGISDEDSLARRQRTRDQWLKQTFDEADKNGDGSLSIGEVQLLHKLNVNLPQRV	128
Qy	207	KQMFREADTDDHQGTLGFEFCAFYKMMSTRRDLYLLMLTYSNHKDHLDAASLQRFLOVE	266
Db	129	KQMFREADTDDHQGTLGFEFCAFYKMMSTRRDLYLLMLTYSNHKDHLDAASLQRFLOVE	188
Qy	267	QKMAGVTLESCQDII EQFEPCPENKSKGLLGIDGFTNYTRSPAGDIFNPEHHHVHQM	326
Db	189	QKMAGVTLESCQDII EQFEPCPENKSKGLLGIDGFTNYTRSPAGDIFNPEHHHVHQM	248
Qy	327	PLSHYFITSSHNTYLVGDQLMSQSRVDMYAWVLQAGCRCVEVDCWDGPDGEPVHHGYTL	386
Db	249	PLSHYFITSSHNTYLVGDQLMSQSRVDMYAWVLQAGCRCVEVDCWDGPDGEPVHHGYTL	308
Qy	387	TSKILFKDVIETINKYAFIKNEYPVILSIENHCSVIQQKKMAQYLTDLGDKLDLSSVSS	446
Db	309	TSKILFKDVIETINKYAFIKNEYPVILSIENHCSVIQQKKMAQYLTDLGDKLDLSSVSS	368
Qy	447	EDATTLPSQMLKGKILVKGKKLPANISEDAAEEGEVSEDSADEIDDDCKLLNGDASTNR	506
Db	369	EDATTLPSQMLKGKILVKGKKLPANISEDAAEEGEVSEDSADEIDDDCKLLNGDASTNR	428
Qy	507	KRVENTAKRKLD SLIKESKIRDCEDPNNFVS VTLSPSGKLGRKSKAEEDVESGEDAGASR	566
Db	429	KRVENTAKRKLD SLIKESKIRDCEDPNNFVS VTLSPSGKLGRKSKAEEDVESGEDAGASR	488
Qy	567	RNGRLVVGVSFSRRKKKGSKLKKAA SVEEGDEGQDSPGGQSRGATRQKKTMKLSRALSDLV	626
Db	489	RNGRLVVGVSFSRRKKKGSKLKKAA SVEEGDEGQDSPGGQSRGATRQKKTMKLSRALSDLV	548
Qy	627	KYTKSVATHDI EMEAASSWQVSSFSETKAHQILQQKPAQYLRFNQQQLSRIYPSSYRVDS	686
Db	549	KYTKSVATHDI EMEAASSWQVSSFSETKAHQILQQKPAQYLRFNQQQLSRIYPSSYRVDS	608
Qy	687	SNYNPQPFWNAGCQMVALNYQSEGRMLQLNRAKFSANGGCGYVLKPGCMCQGVFNPNSED	746
Db	609	SNYNPQPFWNAGCQMVALNYQSEGRMLQLNRAKFSANGGCGYVLKPGCMCQGVFNPNSED	668
Qy	747	PLPGQLKKQLVLR IISGQQLPKPRDSMLGDRGEI IDPFVEVEI IGLPVDCSREQTRVDD	806
Db	669	PLPGQLKKQLVLR IISGQQLPKPRDSMLGDRGEI IDPFVEVEI IGLPVDCSREQTRVDD	728
Qy	807	NGFNPTWEETLVFMVHMP EIALVRFLVWDHDP IGRDFIGQRTLAFSSMMPGYRHVYLEGM	866
Db	729	NGFNPTWEETLVFMVHMP EIALVRFLVWDHDP IGRDFIGQRTLAFSSMMPGYRHVYLEGM	788

Qy	867	EEASIFVHVAVSDISGKVKQALGLKGLFLRGPKPGSLD SHAAGRPPARPSVSQRILRRTA	926
Db	789	EEASIFVHVAVSDISGKVKQVLGLKGLFLRGPKPGSLD SHAAGRPPARPSVSQRILRRTA	848
Qy	927	SAPTKSQKPGRRGFPFELVLGTRDTGSKGVADDVVP GP GPAP EAPAQEGPGSGSPRGKAP	986
Db	849	SAPTKSQKPGRRGFPFELVLGTRDTGSKGVADDVVP GP GPAP EAPAQEGPGSGSPRGKAP	908
Qy	987	AAVAEKSPVRVRPPRVL DGP GPAGMAATCMKCVV GSCAGVNTGGLQ RERPPSPGPASRQA	1046
Db	909	AAVAEKSPVRVRPLRVL DGP GPAGMAATCMKCVV GSCAGVNTGGLQ RERPPSPGPASRQA	968
Qy	1047	AIRQQPRARADSLGAPCCGLDPHAI PGRSREAPKGP GAWRQGP GSGSMS SDSSSPDSPG	1106
Db	969	AIRQQPRARADSLGAPCCGLDPHAI PGRSREAPKGP GAWRQGP GSGSMS SDSSSPDSPG	1028
Qy	1107	I PERSPRWPEGACRQPGALQ GEMSALFAQLEEIRSKSPMFSAGKPLLPCVVLP HAPGMA	1166
Db	1029	I PERSPRWPEGACRQPGALQ GEMSALFAQLEEIRSKSPMFSAGKPLLPCVVLP HAPGMA	1088
Qy	1167	GPGSPAAASAWTVSPRVLVLVALYPWHCLRG TLLPWLACGP	1207
Db	1089	GPGSPAAASAWTVSPRVLVLVALYPWHCLRG TLLPWLACGP	1129

## RESULT 3

Q5TA87\_HUMAN

ID Q5TA87\_HUMAN PRELIMINARY; PRT; 1058 AA.

AC Q5TA87;

DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.

DT 21-DEC-2004, sequence version 1.

DT 07-FEB-2006, entry version 9.

DE Novel protein.

GN Name=RP3-395M20.1; ORFNames=RP3-395M20.1-001;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Moore M.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

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CC -----

DR EMBL; AL139246; CAI20407.1; -; Genomic\_DNA.

DR Ensembl; ENSG00000149527; Homo sapiens.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0004435; F:phosphoinositide phospholipase C activity; IEA.

DR GO; GO:0007242; P:intracellular signaling cascade; IEA.

DR GO; GO:0006629; P:lipid metabolism; IEA.

DR InterPro; IPR000008; C2.

DR InterPro; IPR011992; EF-Hand\_type.

DR InterPro; IPR002048; EF\_hand\_Ca\_bd.

DR InterPro; IPR001192; PI\_PLC.

DR InterPro; IPR000909; PI\_PLC\_X.

DR InterPro; IPR001711; PI\_PLC\_Y.

DR Pfam; PF00168; C2; 1.

DR Pfam; PF00036; efhand; 3.

DR Pfam; PF00388; PI-PLC-X; 1.

DR Pfam; PF00387; PI-PLC-Y; 1.

DR PRINTS; PR00360; C2DOMAIN.

DR PRINTS; PR00390; PHPHLIPASEC.

DR ProDom; PD000012; EF-hand; 1.

DR ProDom; PD001202; PI\_PLC\_Y; 2.

DR SMART; SM00239; C2; 1.

DR SMART; SM00054; EFh; 2.

DR SMART; SM00148; PLCXc; 1.

DR SMART; SM00149; PLCYc; 1.

DR PROSITE; PS50004; C2\_DOMAIN; 1.

DR PROSITE; PS00018; EF\_HAND\_1; UNKNOWN\_1.

DR PROSITE; PS50222; EF\_HAND\_2; 2.

DR PROSITE; PS50007; PIPLC\_X\_DOMAIN; 1.

DR PROSITE; PS50008; PIPLC\_Y\_DOMAIN; 1.

SQ SEQUENCE 1058 AA; 115520 MW; D923C4349BE6BD17 CRC64;

Query Match 87.4%; Score 5576; DB 2; Length 1058;

Best Local Similarity 100.0%; Pred. No. 1.2e-260;

Matches 1058; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 150 MAGISDEDSLARRQRTDQWLKQTFDEADKNGDGSLSIGEVLLHKLNVNLPRQVRVKQM 209

|||||

Db 1 MAGISDEDSLARRQRTDQWLKQTFDEADKNGDGSLSIGEVLLHKLNVNLPRQVRVKQM 60

Qy	210	FREADTDDHQGT	LGFE	EFCAF	YKMM	STRD	LYLL	MLTY	SNHK	DHLD	AASL	QRF	LQVE	QKM	269
Db	61	FREADTDDHQGT	LGFE	EFCAF	YKMM	STRD	LYLL	MLTY	SNHK	DHLD	AASL	QRF	LQVE	QKM	120
Qy	270	AGVTLESCQDI	IEQF	EPCP	ENKSK	GLLG	IDGF	TNYTR	SPAG	DIFN	PEHH	VHQD	MTQP	LS	329
Db	121	AGVTLESCQDI	IEQF	EPCP	ENKSK	GLLG	IDGF	TNYTR	SPAG	DIFN	PEHH	VHQD	MTQP	LS	180
Qy	330	HYFITSSHNTY	LVGD	QLMS	QSRV	DMYAW	VLQAG	CRCV	EVDC	WDGP	DGEPI	VHHG	YTLT	SK	389
Db	181	HYFITSSHNTY	LVGD	QLMS	QSRV	DMYAW	VLQAG	CRCV	EVDC	WDGP	DGEPI	VHHG	YTLT	SK	240
Qy	390	ILFKDVIETIN	KYAF	IKNE	YPVIL	SIEN	HCSV	IQKK	MAQY	LT	ILGD	KL	DLSS	VSS	449
Db	241	ILFKDVIETIN	KYAF	IKNE	YPVIL	SIEN	HCSV	IQKK	MAQY	LT	ILGD	KL	DLSS	VSS	300
Qy	450	TTLPSQMLKGI	LVKG	KKLP	PANIS	EDAE	EGEV	SDEDS	ADEI	DDCK	LLNG	DAST	NRKR	V	509
Db	301	TTLPSQMLKGI	LVKG	KKLP	PANIS	EDAE	EGEV	SDEDS	ADEI	DDCK	LLNG	DAST	NRKR	V	360
Qy	510	ENTAKRKLD	SLIKE	SKIRD	CEDP	NNFS	VSTLS	PSGK	LGRK	SKAE	EDVE	SGED	AGAS	RRNG	569
Db	361	ENTAKRKLD	SLIKE	SKIRD	CEDP	NNFS	VSTLS	PSGK	LGRK	SKAE	EDVE	SGED	AGAS	RRNG	420
Qy	570	RLVVGFSFRR	KKKGS	KLKKA	ASVE	EGDE	GQDS	PGGQ	SRGAT	RQKKT	MKLS	RALS	DLVK	YKT	629
Db	421	RLVVGFSFRR	KKKGS	KLKKA	ASVE	EGDE	GQDS	PGGQ	SRGAT	RQKKT	MKLS	RALS	DLVK	YKT	480
Qy	630	KSVATHDIE	MEAAS	SWQVS	SFSET	KAHQ	ILQQ	KPAQ	YLRFN	QQQL	SRIY	PSSY	RVDSS	SNY	689
Db	481	KSVATHDIE	MEAAS	SWQVS	SFSET	KAHQ	ILQQ	KPAQ	YLRFN	QQQL	SRIY	PSSY	RVDSS	SNY	540
Qy	690	NPQPFWNAG	CQMV	ALNY	QSEGR	MLQL	NRAK	FSAN	GGCG	YVLK	PGCM	CQGV	FNPNS	EDPLP	749
Db	541	NPQPFWNAG	CQMV	ALNY	QSEGR	MLQL	NRAK	FSAN	GGCG	YVLK	PGCM	CQGV	FNPNS	EDPLP	600
Qy	750	GQLKKQLVL	RIIS	GQQL	PKPR	DSML	GDRGE	IIDP	FVEVE	EIIG	LPVD	CSRE	QTRV	VDDNGF	809
Db	601	GQLKKQLVL	RIIS	GQQL	PKPR	DSML	GDRGE	IIDP	FVEVE	EIIG	LPVD	CSRE	QTRV	VDDNGF	660
Qy	810	NPTWEETLV	FVMH	MP	PEIAL	VRFL	VWDH	DP	IGRDF	IGQRT	LAFSS	MMPG	YR	HVYLEG	869
Db	661	NPTWEETLV	FVMH	MP	PEIAL	VRFL	VWDH	DP	IGRDF	IGQRT	LAFSS	MMPG	YR	HVYLEG	720
Qy	870	SIFVHVAVSD	ISGK	VKQAL	GLKGL	FLRG	PKPG	SLD	SHAAG	RPPAR	PSVS	QRI	LRRT	ASAP	929
Db	721	SIFVHVAVSD	ISGK	VKQAL	GLKGL	FLRG	PKPG	SLD	SHAAG	RPPAR	PSVS	QRI	LRRT	ASAP	780
Qy	930	TKSQKPGRR	GFPE	LVLG	TRDT	GSKG	VADD	VVPP	PGPA	PEAPA	QEGP	SGSG	SPRG	KAPAAV	989
Db	781	TKSQKPGRR	GFPE	LVLG	TRDT	GSKG	VADD	VVPP	PGPA	PEAPA	QEGP	SGSG	SPRG	KAPAAV	840
Qy	990	AEKSPVRVR	PPRV	LDG	PGPA	GMAAT	CMKC	VVG	SCAG	VNTG	GLQR	ERPP	SPGP	ASRQAAIR	1049
Db	841	AEKSPVRVR	PPRV	LDG	PGPA	GMAAT	CMKC	VVG	SCAG	VNTG	GLQR	ERPP	SPGP	ASRQAAIR	900
Qy	1050	QQPRARADSL	GAPCC	GLDP	HAIP	GRS	REAP	KPGP	AWRQ	GP	GGSG	SMSS	DSSSP	DSPGIPE	1109
Db	901	QQPRARADSL	GAPCC	GLDP	HAIP	GRS	REAP	KPGP	AWRQ	GP	GGSG	SMSS	DSSSP	DSPGIPE	960
Qy	1110	RSPRWPEGAC	RQPG	ALQ	GEM	SALF	AQK	LEEIR	SKSP	MF	SAGK	PLLPC	VVLPH	APGMAGPG	1169

```

          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 RSPRWPEGACRQPGALQGEMSALFAQKLEEEIRSKSPMFSAGKPLLPCVVLPHPAGMAGPG 1020
Qy      1170 SPAAASAWTVSPRVLVLVALYPWHCLRGTTLLPWLACGP 1207
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 SPAAASAWTVSPRVLVLVALYPWHCLRGTTLLPWLACGP 1058
```